US-1380
SEQUENCE LISTING

<110> IZUI, Masako
      SUGIMOTO, Masakazu
      KURAHASHI, Osamu
      NAKAMATSU, TSUYOSHI

<120> DNA Encoding Sucrose PTS Enzyme II

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<140> US 10/019,284
<141> 2002-01-02

<150> JP 11-189512
<151> 1999-07-02

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<170> PatentIn Ver. 2.0

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Met Asp His Lys Asp Leu Ala Gln Arg Ile Leu Arg Asp Ile Gly Gly
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Glu Asp Asn Ile Val Ala Ala Ala His Cys Ala Thr Arg Leu Arg Leu
                 20                  25                  30
gtg ctc aaa gac acc aag gat gtg gat cgc caa agt ctg gat gat gat 3922
Val Leu Lys Asp Thr Lys Asp Val Asp Arg Gln Ser Leu Asp Asp Asp
         35                  40                  45
cca gat ctg aaa ggc acc ttt gaa act ggc ggc atg ttc cag atc atc 3970
Pro Asp Leu Lys Gly Thr Phe Glu Thr Gly Gly Met Phe Gln Ile Ile
     50                  55                  60
gtc ggg cca ggc gat gtg gat cat gtt ttc aaa gaa ctc gat gac gca 4018
Val Gly Pro Gly Asp Val Asp His Val Phe Lys Glu Leu Asp Asp Ala
 65                  70                  75                  80
acc tcc aaa gac atc gct gtg tcc aca gag cag ctc aaa gat gtt gtg 4066
Thr Ser Lys Asp Ile Ala Val Ser Thr Glu Gln Leu Lys Asp Val Val
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Ala Asn Asn Ala Asn Trp Phe Ser Arg Ala Val Lys Val Leu Ala Asp
             100                 105                 110
att ttc gtc ccg ctg att cca atc ttg gtt ggt ggc ggt ctg ctc atg   4162
Ile Phe Val Pro Leu Ile Pro Ile Leu Val Gly Gly Gly Leu Leu Met
             115                 120                 125
gct atc aac aat gtg ttg gtt gcg cag gat ctg ttc ggt ccg caa tca   4210
Ala Ile Asn Asn Val Leu Val Ala Gln Asp Leu Phe Gly Pro Gln Ser
     130                 135                 140
ctg gtg gag atg ttc cct cag atc agc ggt gtt gct gag atg atc aac   4258
Leu Val Glu Met Phe Pro Gln Ile Ser Gly Val Ala Glu Met Ile Asn
145                 150                 155                 160
ctg atg gca tct gcg ccg ttc gcg ttc ttg cca gtg ttg gtt ggt ttc   4306
Leu Met Ala Ser Ala Pro Phe Ala Phe Leu Pro Val Leu Val Gly Phe
                 165                 170                 175
acc gca acc aag cgt ttc ggt ggc aat gag ttc ctg ggc gcc ggc att   4354
Thr Ala Thr Lys Arg Phe Gly Gly Asn Glu Phe Leu Gly Ala Gly Ile
             180                 185                 190
ggt atg gcg atg gtg ttc cca acc ctg gtt aac ggc tac gac gtg gcc   4402
Gly Met Ala Met Val Phe Pro Thr Leu Val Asn Gly Tyr Asp Val Ala
             195                 200                 205
gcc acc atg acc gcg ggc gaa atg cca atg tgg tcc ctg ttt ggt ttg   4450
Ala Thr Met Thr Ala Gly Glu Met Pro Met Trp Ser Leu Phe Gly Leu
     210                 215                 220
gat gtt gct caa gct ggt tac cag ggc acc gtg ctt cct gtg ctg gtg   4498
Asp Val Ala Gln Ala Gly Tyr Gln Gly Thr Val Leu Pro Val Leu Val
225                 230                 235                 240
gtc tct tgg att ctg gca acg atc gag aag ttc ctg cac aag cga ctc   4546
Val Ser Trp Ile Leu Ala Thr Ile Glu Lys Phe Leu His Lys Arg Leu
                 245                 250                 255
atg ggc act gca gac ttc ctg atc acc cca gtg ttg act ctg ctg ctc   4594
Met Gly Thr Ala Asp Phe Leu Ile Thr Pro Val Leu Thr Leu Leu Leu
             260                 265                 270
acc ggc ttc ctt acg ttc att gct att ggt cca gca atg cgc tgg gtg   4642
Thr Gly Phe Leu Thr Phe Ile Ala Ile Gly Pro Ala Met Arg Trp Val
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ggt gac ttg ctg gca cac ggt ctg cag gga ctc tat gat ttc ggt ggt   4690
Gly Asp Leu Leu Ala His Gly Leu Gln Gly Leu Tyr Asp Phe Gly Gly
     290                 295                 300
cca gtc ggc ggt ctg ctt ttc ggt ctg gtc tac tca cca atc gtt atc   4738
Pro Val Gly Gly Leu Leu Phe Gly Leu Val Tyr Ser Pro Ile Val Ile
305                 310                 315                 320
act ggt ctg cac cag tcc ttc ccg cca att gag ctg gag ctg ttc aac   4786
Thr Gly Leu His Gln Ser Phe Pro Pro Ile Glu Leu Glu Leu Phe Asn
                 325                 330                 335
cag ggt gga tcc ttc atc ttc gca acc gca tcc atg gcc aat atc gcg   4834
Gln Gly Gly Ser Phe Ile Phe Ala Thr Ala Ser Met Ala Asn Ile Ala
             340                 345                 350
cag ggt gca gca tgt ttg gca gtg ttc ttc cta gcg aag agt gaa aag   4882
Gln Gly Ala Ala Cys Leu Ala Val Phe Phe Leu Ala Lys Ser Glu Lys
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ctc aag ggc ctt gca ggt gct tca ggt gtc tcc gct gtt ctt ggt att   4930
Leu Lys Gly Leu Ala Gly Ala Ser Gly Val Ser Ala Val Leu Gly Ile
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Thr Glu Pro Ala Ile Phe Gly Val Asn Leu Arg Leu Arg Trp Pro Phe
385                    390                    395                    400
tac att ggt atc ggt acc gca gct atc ggt ggc gct ttg att gca ctc    5026
Tyr Ile Gly Ile Gly Thr Ala Ala Ile Gly Gly Ala Leu Ile Ala Leu
                       405                    410                    415
ttt gat atc aag gca gtt gcg ttg ggc gct gca ggt ttc ttg ggt gtt    5074
Phe Asp Ile Lys Ala Val Ala Leu Gly Ala Ala Gly Phe Leu Gly Val
                420                    425                    430
gtt tct att gat gct cca gat atg gtc atg ttc ttg gtt tgc gcg gta    5122
Val Ser Ile Asp Ala Pro Asp Met Val Met Phe Leu Val Cys Ala Val
                435                    440                    445
gtt acc ttt gtc atc gca ttc ggc gca gcg att gct tat ggc ctt tac    5170
Val Thr Phe Val Ile Ala Phe Gly Ala Ala Ile Ala Tyr Gly Leu Tyr
                450                    455                    460
ttg gtt cgc cgc aac ggc agc att gat cca gat gca acc gct gct cca    5218
Leu Val Arg Arg Asn Gly Ser Ile Asp Pro Asp Ala Thr Ala Ala Pro
465                    470                    475                    480
gtg cct gca gga acg acc aaa gcc gaa gca gaa gca ccc gca gaa ttt    5266
Val Pro Ala Gly Thr Thr Lys Ala Glu Ala Glu Ala Pro Ala Glu Phe
                       485                    490                    495
tca aac gat tcc acc atc atc cag gca cct ttg acc ggt gaa gct atc    5314
Ser Asn Asp Ser Thr Ile Ile Gln Ala Pro Leu Thr Gly Glu Ala Ile
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gca ctg agc agc gtc agc gat gcc atg ttt gcc agc gga aag ctt ggc    5362
Ala Leu Ser Ser Val Ser Asp Ala Met Phe Ala Ser Gly Lys Leu Gly
                515                    520                    525
tca ggt gtt gcg atc gtc ccc acc aag ggg cag ctg gtt tca cca gtg    5410
Ser Gly Val Ala Ile Val Pro Thr Lys Gly Gln Leu Val Ser Pro Val
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agc gga aag atc gtg gtg gcc ttc cca tct ggt cac gct ttc gca gtc    5458
Ser Gly Lys Ile Val Val Ala Phe Pro Ser Gly His Ala Phe Ala Val
545                    550                    555                    560
cgc act aag gct gag gat ggt tcc aat gtg gat atc ttg atg cac att    5506
Arg Thr Lys Ala Glu Asp Gly Ser Asn Val Asp Ile Leu Met His Ile
                565                    570                    575
ggt ttc gac acc gta aac ctc aac ggc acg cac ttt aac ccg ctg aag    5554
Gly Phe Asp Thr Val Asn Leu Asn Gly Thr His Phe Asn Pro Leu Lys
                580                    585                    590
aag cag ggc gat gaa gtc aaa gca ggg gag ctg ctg tgt gaa ttc gat    5602
Lys Gln Gly Asp Glu Val Lys Ala Gly Glu Leu Leu Cys Glu Phe Asp
                595                    600                    605
att gat gcc att aag gct gca ggt tat gag gta acc acg ccg att gtt    5650
Ile Asp Ala Ile Lys Ala Ala Gly Tyr Glu Val Thr Thr Pro Ile Val
                610                    615                    620
gtt tcg aat tac aag aaa acc gga cct gta aac act tac ggt ttg ggc    5698
Val Ser Asn Tyr Lys Lys Thr Gly Pro Val Asn Thr Tyr Gly Leu Gly
625                    630                    635                    640
gaa att gaa gcg gga gcc aac ctg ctc aac gtc gca aag aaa gaa gcg    5746
Glu Ile Glu Ala Gly Ala Asn Leu Leu Asn Val Ala Lys Lys Glu Ala
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gtg cca gca aca cca taagttgaaa ccttgagtgt cgcacacag gttagactag    5801
Val Pro Ala Thr Pro
                660
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<213> Brevibacterium lactofermentum

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        35                  40                  45
Pro Asp Leu Lys Gly Thr Phe Glu Thr Gly Gly Met Phe Gln Ile Ile
     50                  55                  60
Val Gly Pro Gly Asp Val Asp His Val Phe Lys Glu Leu Asp Asp Ala
65                  70                  75                  80
Thr Ser Lys Asp Ile Ala Val Ser Thr Glu Gln Leu Lys Asp Val Val
                85                  90                  95
Ala Asn Asn Ala Asn Trp Phe Ser Arg Ala Val Lys Val Leu Ala Asp
            100                 105                 110
Ile Phe Val Pro Leu Ile Pro Ile Leu Val Gly Gly Gly Leu Leu Met
        115                 120                 125
Ala Ile Asn Asn Val Leu Val Ala Gln Asp Leu Phe Gly Pro Gln Ser
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145                 150                 155                 160
Leu Met Ala Ser Ala Pro Phe Ala Phe Leu Pro Val Leu Val Gly Phe
                165                 170                 175
Thr Ala Thr Lys Arg Phe Gly Gly Asn Glu Phe Leu Gly Ala Gly Ile
            180                 185                 190
Gly Met Ala Met Val Phe Pro Thr Leu Val Asn Gly Tyr Asp Val Ala
        195                 200                 205
Ala Thr Met Thr Ala Gly Glu Met Pro Met Trp Ser Leu Phe Gly Leu
210                 215                 220
Asp Val Ala Gln Ala Gly Tyr Gln Gly Thr Val Leu Pro Val Leu Val
225                 230                 235                 240
Val Ser Trp Ile Leu Ala Thr Ile Glu Lys Phe Leu His Lys Arg Leu
                245                 250                 255
Met Gly Thr Ala Asp Phe Leu Ile Thr Pro Val Leu Thr Leu Leu Leu
            260                 265                 270
Thr Gly Phe Leu Thr Phe Ile Ala Ile Gly Pro Ala Met Arg Trp Val
        275                 280                 285
Gly Asp Leu Leu Ala His Gly Leu Gln Gly Leu Tyr Asp Phe Gly Gly
        290                 295                 300
Pro Val Gly Gly Leu Leu Phe Gly Leu Val Tyr Ser Pro Ile Val Ile
305                 310                 315                 320
Thr Gly Leu His Gln Ser Phe Pro Pro Ile Glu Leu Glu Leu Phe Asn
            325                 330                 335
Gln Gly Gly Ser Phe Ile Phe Ala Thr Ala Ser Met Ala Asn Ile Ala
            340                 345                 350
Gln Gly Ala Ala Cys Leu Ala Val Phe Phe Leu Ala Lys Ser Glu Lys
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385                     390                 395                 400
Tyr Ile Gly Ile Gly Thr Ala Ala Ile Gly Gly Ala Leu Ile Ala Leu
                    405                 410                 415
Phe Asp Ile Lys Ala Val Ala Leu Gly Ala Ala Gly Phe Leu Gly Val
                420                 425                 430
Val Ser Ile Asp Ala Pro Asp Met Val Met Phe Leu Val Cys Ala Val
            435                 440                 445
Val Thr Phe Val Ile Ala Phe Gly Ala Ala Ile Ala Tyr Gly Leu Tyr
        450                 455                 460
Leu Val Arg Arg Asn Gly Ser Ile Asp Pro Asp Ala Thr Ala Ala Pro
465                 470                 475                 480
Val Pro Ala Gly Thr Thr Lys Ala Glu Ala Glu Ala Pro Ala Glu Phe
                485                 490                 495
Ser Asn Asp Ser Thr Ile Ile Gln Ala Pro Leu Thr Gly Glu Ala Ile
            500                 505                 510
Ala Leu Ser Ser Val Ser Asp Ala Met Phe Ala Ser Gly Lys Leu Gly
        515                 520                 525
Ser Gly Val Ala Ile Val Pro Thr Lys Gly Gln Leu Val Ser Pro Val
    530                 535                 540
Ser Gly Lys Ile Val Val Ala Phe Pro Ser Gly His Ala Phe Ala Val
545                 550                 555                 560
Arg Thr Lys Ala Glu Asp Gly Ser Asn Val Asp Ile Leu Met His Ile
                565                 570                 575
Gly Phe Asp Thr Val Asn Leu Asn Gly Thr His Phe Asn Pro Leu Lys
            580                 585                 590
Lys Gln Gly Asp Glu Val Lys Ala Gly Glu Leu Leu Cys Glu Phe Asp
        595                 600                 605
Ile Asp Ala Ile Lys Ala Ala Gly Tyr Glu Val Thr Thr Pro Ile Val
    610                 615                 620
Val Ser Asn Tyr Lys Lys Thr Gly Pro Val Asn Thr Tyr Gly Leu Gly
625                 630                 635                 640
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            645                 650                 655
Val Pro Ala Thr Pro
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<213> Artificial Sequence

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<221> misc_feature
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<400> 3
gtacatattg tcgttagaac gcgtaatacg actcactata ggga 44

<210> 4
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: EcoRI cassette

<220>
<221> misc_feature
<222> (47)
<223> complementary strand extends a single strand having
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<210> 5
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
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<220>
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<222> (46)
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<210> 6
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<212> DNA
<213> Artificial Sequence

<220>
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<220>
<221> misc_feature
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<210> 7

<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: SalI cassette

<220>
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<222> (47)
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<211> 47
<212> DNA
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<220>
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<220>
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<222> (47)
<223> complementary strand extends a single strand having
       a sequence of 3'-gatc-5' at this position in the
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<400> 8
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<210> 9
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
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<400> 9
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<210> 10
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
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<400> 10

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<210> 11
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<212> DNA
<213> Artificial Sequence

<220>
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<400> 11
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<210> 12
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for PCR

<400> 12
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<220>
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<400> 13
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<220>
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<212> DNA
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<220>
<223> Description of Artificial Sequence: primer for PCR

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<212> DNA
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<220>
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<210> 17
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for PCR

<400> 17
gcagcgtcag cgatgccatg tttgc                                    25

<210> 18
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for PCR

<400> 18
gcttggctca ggtgttgcga tcgtc                                    25

<210> 19
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: cassette
      primer 1

<400> 19
gtacatattg tcgttagaac gcggtaatac gactca                        36

<210> 20
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: cassette
      primer 2
```

<400> 20
cgttagaacg cgtaatacga ctcactatag ggaga   35

<210> 21
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for PCR

<400> 21
cgctactgct gaacgaacat gtcc   24